Encoding of pre-selected compartments produces large SNR and speed advantages for ^{31}P MRS

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Introduction: Scan-time and signal-to-noise ratio (SNR) are major problems for MRS of low-concentration metabolites. Because SNR is proportional to voxel size, matching the voxel to the desired anatomical compartment *a priori* yields the best SNR. By comparison, adding signals from smaller chemical shift imaging (CSI) voxels post-acquisition yields less SNR by a factor of {compartment size/CSI voxel size}$^{1/2}$, due to the way noise adds [1]. While SLIM [2], GSLIM [3] and SLOOP [4] approaches could permit localization if pre-selected compartments and reduced CSI encoding sets were used, the prescribing of compartments and tailoring of gradient-encoding steps at the time of acquisition–central to realizing the full SNR gain–has, to our knowledge, never been realized. Here, assuming that spectra from each compartment are fairly homogeneous, we use a linear algebraic model (LAM) and matrix analysis to reconstruct average spectra from pre-selected compartments acquired with a reduced number of CSI phase-encoding steps comparable to the number of compartments. By applying just a fraction of the CSI phase-encoding steps–those with high-SNR close to central k-space–we demonstrate a ~2.4-fold gain in 3T ^{31}P MRS SNR in the human leg, and a ~4-fold decrease in scan-time in the heart, as compared to conventional 1D CSI done with the same volume size and gradient increment.

Theory: The mathematical equation for conventional 1D CSI is: $S_{M*N} = PE_{M*M} * \rho_{M*N}$ where S is the known signal matrix, PE is the phase encoding Fourier transform operator and ρ are the unknown spectra. M is the number of phase encoding steps (e.g., M=16) and N is the number of time-domain data points (e.g., N=512). In 1D CSI, M spectra are reconstructed from M signals. If we incorporate the *a priori* assumption that there are C (<<M) compartments, the number of measurements reduces significantly to M' with C≤M'≤M. Introducing a new matrix, *b*, to reduce the number of unknown spectra from M to M' yields an equation for this SLIM-related LAM method: $S_{M*N} = PE_{M*M} * {b^{-1}}_{M*M} * b_{M*M} * \rho_{M*N}$, where *b* is used to eliminate identical rows in the ρ matrix depending on the spatial extent and position of each compartment. The elimination of identical rows reduces the dimension of $(b_{M*M} * \rho_{M*N})$ from M to C, for which a reduced number of acquisitions M' ≥C will suffice. After dimensional reduction, we have $S^*_{M'*N} = PE^*_{M'*C} * \rho^*_{C*N}$ where $PE^*_{M'*C}$ is a submatrix of $(PE_{M*M} * {b^{-1}}_{M*M})$, ρ^*_{C*N} is a submatrix of $(b_{M*M} * \rho_{M*N})$ and $S^*_{M'*N}$ is a submatrix of S_{M*N}. Solution of this new matrix equation results in a set of spectra, each closely approximating the average spectrum from each 1D compartment.

Experiment: The method is implemented as follows: (i) Acquire a proton image; (ii) Segment the image into C compartments; (iii) Apply M' phase encodes; and (iv) Reconstruct the spectra using LAM.

^{31}P MRS experiments were done on phantoms, the human leg, and the human heart using a 3T Philips system with a 17cm/8cm transmit/receive ^{31}P coil set. Leg studies were done with a 300mM H_3PO_4 phantom on top. SLIM/LAM is compared with CSI performed with the same total scan time and gradient step increments (CSI encoding steps, -8,-7,-6,-5, -4,-3,-2,-1,0,1,2,3,4,5,6,7; for SLIM-related LAM encoding steps were -2,-1,0,1 repeated 4 times). Cardiac studies were ECG-triggered using LAM encoding steps of (-2,-1,0,1) without repeats for a 4-fold gain in speed.

Results: The spectrum for the same-sized leg compartment from CSI (averaging n=6 slices) and LAM (same volume) are shown in Fig. 1 normalized to constant noise. The SLIM-LAM approach yielded 2.4 times better SNR than CSI and negligible bleed from the H_3PO_4. Fig. 2 shows ^{31}P heart spectra from a 16-step1DCSI (averaging 4 slices), and 4-step LAM from the same volume. SNR is comparable but the LAM spectrum was acquired 4-times faster.

Fig. 1: Human leg ^{31}P MRS (same volume & scan time) LAM vs. CSI.

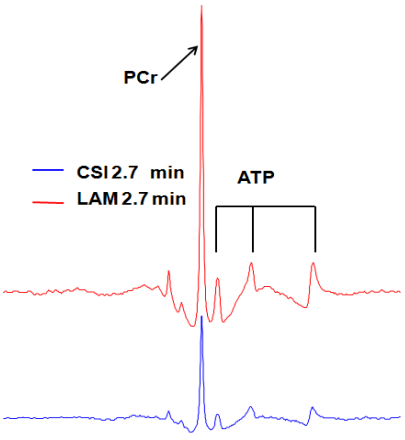
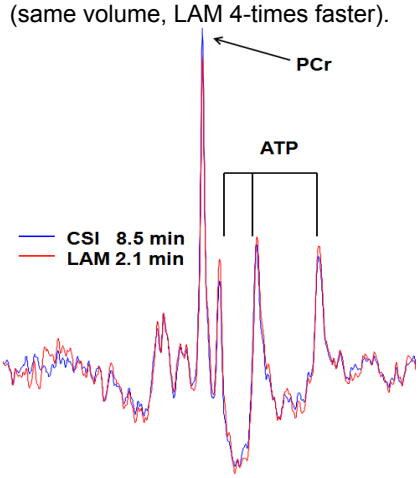


Fig. 2: ^{31}P MRS from human heart, (same volume, LAM 4-times faster).



Conclusion: This LAM method yields spectra not discernable from the average of pre-selected compartments in the sample, with dramatic gains in SNR and/or reductions in scan time compared to conventional CSI.

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Grant support: R01 EB07829, HL056882, HL61912